

In the Claims

Rewrite claims 2, 13, 20-27 and 30 as follows:

2. (thrice amended) A process for the preparation of a transgenic plant, which process comprises:

(i) transforming a plant cell with a chimaeric gene comprising (a) a promoter operably linked to (b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes for an enzyme selected from the group consisting of phosphofructokinase, pyruvate kinase, acid invertase, starch synthase, [adenine] adenosine diphosphoglucose pyrophosphorylase, sucrose synthase, [6-phospho-fructokinase] 6- phosphofructokinase (pyrophosphate) and sucrose phosphate synthetase; whereby there is caused a modification of the amount of a metabolic intermediate in glycolysis or in a pathway for the synthesis or degradation of starch, sucrose or reducing sugar, and

(ii) regenerating a plant from the transformed cell.

*E 2*

13. (thrice amended) A transgenic plant which harbors in its cells a chimaeric gene which comprises;

(a) a promoter operably linked to

(b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes an enzyme selected from the group consisting of phosphofructokinase, pyruvate kinase, acid invertase, starch synthase, 6-phosphofructokinase (pyrophosphate), [adenine] adenosine diphosphoglucose [diphosphoglucose] pyrophosphorylase, sucrose synthase and sucrose phosphate synthetase; and which is capable of being expressed in the cells of the plant thus to cause a modification of the amount of a metabolic intermediate in glycolysis or in a pathway for the synthesis or degradation of starch, sucrose or reducing sugar.

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20. (twice amended) A transgenic potato plant which harbors in its cells a chimaeric gene, which comprises;

(a) a promoter operably linked to

(b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes [adenine] adenosine diphosphoglucose pyrophosphorylase [pyrophosphorylase]; said gene being capable of expression in the cells of the transgenic potato plant.

21. (twice amended) A transgenic potato plant according to claim 20 wherein the [fragment] gene also comprises a coding sequence which encodes for a second enzyme.

22. (twice amended) A process according to claim 2,  
wherein the [fragment] gene encodes for [2] two or more of  
the enzymes selected.

23. (twice amended) A chimaeric gene ~~as defined~~  
~~in~~ according to claim [1<sup>9</sup>] 2 wherein the [fragment] gene  
encodes for [2] two or more of the enzymes selected.

24. (twice amended) A transgenic plant according to claim 13 wherein the [fragment] gene encodes for [2] two or more of the enzymes selected.

25. (twice amended) A transgenic plant which harbors in its cells a chimaeric gene, which comprises;

(a) a promoter operably linked to

(b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes for phosphofructokinase and the gene comprising a coding sequence encoding for a second enzyme selected from the group consisting of pyruvate kinase, acid invertase, starch synthase, [adenine diphosphoglucose] adenosine diphosphoglucose pyrophosphorylase,

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sucrose synthase, 6-phosphofructokinase (pyrophosphate) and sucrose phosphate synthetase;

said gene being capable of being expressed in the cells of the transgenic plant.

26. (twice amended) A transgenic potato plant which harbors in its cells a chimaeric gene, which comprises:

(a) a promoter operably linked to  
(b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes [adenine diphosphoglucone] adenosine diphosphoglucose pyrophosphorylase and the gene comprising a coding sequence encoding for a second enzyme selected from the group consisting of phosphofructokinase, pyruvate kinase, acid invertase, starch synthase, sucrose synthase, 6-phosphofructokinase (pyrophosphate) and sucrose phosphate synthetase; said gene being capable of being expressed in the cells of the transgenic potato plant.

27. (amended) A transgenic potato plant which harbors in its cells a chimaeric gene, which comprises:

(a) a promoter operably linked to  
(b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes for acid invertase, and the gene comprising a coding sequence encoding for a second enzyme, said gene being capable of expression in the cells of the transgenic potato plant.

30. (amended) A transgenic plant which harbors in its cells a chimaeric gene comprising;

(a) a promoter operably linked to  
(b) a deoxyribonucleic acid fragment which comprises a coding sequence for an enzyme in the pre-existing plant pathway of glycolysis or the synthesis or degradation of starch, sucrose or reducing sugar, and [the product] of which causes modification of the amount of metabolic intermediate in glycolysis or in a pathway for the synthesis or degradation of starch, sucrose or reducing sugar.

Enter new claims 31-59, inclusive, as follows:

31. The process of claim 2 wherein the enzyme selected is phosphofructokinase.

32. The process of claim 2 wherein the enzyme selected is pyruvate kinase.

33. The process of claim 2 wherein the enzyme selected is starch synthase.

34. The process of claim 2 wherein the enzyme selected is adenosine diphosphoglucose pyrophosphorylase.

35. The process of claim 2 wherein the enzyme selected is sucrose synthase.

36. The process of claim 2 wherein the enzyme selected is acid invertase.

37. The process of claim 2 wherein the enzyme selected is 6-phosphofructokinase (pyrophosphate).

38. The process of claim 2 wherein the enzyme selected is sucrose phosphate synthetase.

39. The plant of claim 13 wherein the enzyme selected is phosphofructokinase.

40. The plant of claim 13 wherein the enzyme selected is pyruvate kinase.

41. The plant of claim 13 wherein the enzyme selected is starch synthase.

42. The plant of claim 13 wherein the enzyme selected is acid invertase.

43. The plant of claim 13 wherein the enzyme selected is adenosine diphosphoglucose pyrophosphorylase.

44. The plant of claim 13 wherein the enzyme selected is sucrose synthase.

45. The plant of claim 13 wherein the enzyme selected is 6-phosphofructokinase (pyrophosphate).

46. The plant of claim 13 wherein the enzyme selected is sucrose phosphate synthetase.

47. A process according to claim 2, wherein said gene comprises a coding sequence encoding for a second enzyme.

48. A process according to claim 2, wherein said fragment is expressed in a tuber of said regenerated plant.

49. A process according to claim 2, wherein said fragment is expressed in a seed of said regenerated plant.

50. A transgenic tuber which harbors in its cells a chimaeric gene which comprises:

(a) a promoter operably linked to  
(b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes an enzyme

selected from the group consisting of phosphofructokinase, pyruvate kinase, acid invertase, starch synthase, 6-phosphofructokinase (pyrophosphate), adenosine diphosphoglucose pyrophosphorylase, sucrose synthase and sucrose phosphate synthetase; and which is capable of being expressed in the cells of the tuber.

*E6*  
51. A transgenic seed which harbors in its cells a chimaeric gene which comprises;

(a) a promoter operably linked to  
(b) a deoxyribonucleic acid fragment comprising a coding sequence which encodes an enzyme selected from the group consisting of phosphofructokinase, pyruvate kinase, acid invertase, starch synthase, 6-phosphofructokinase (pyrophosphate), adenosine diphosphoglucose pyrophosphorylase, sucrose synthase and sucrose phosphate synthetase; and which is capable of being expressed in the cells of the seed.

52. A transgenic plant according to claim 13, wherein the gene encodes for a second enzyme.

53. A transgenic tuber which harbors in its cells a chimaeric gene comprising;

(a) a promoter operably liked to  
(b) a deoxyribonucleic acid fragment which comprises a coding sequence for an enzyme in the pathway of glycolysis or the synthesis or degradation of starch, sucrose or reducing sugar and which causes modification of the amount of a metabolic intermediate in glycolysis or in a pathway for the synthesis or degradation of starch, sucrose or reducing sugar.

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54. A transgenic seed which harbors in its cells a chimaeric gene comprising;

(a) a promoter operably liked to  
(b) a deoxyribonucleic acid fragment which comprises a coding sequence for an enzyme in the pathway of glycolysis or the synthesis or degradation of starch, sucrose or reducing sugar and which causes modification of the amount of a metabolic intermediate in glycolysis or in a pathway for the synthesis or degradation of starch, sucrose or reducing sugar.

55. A transgenic plant according to claim 30, wherein said gene encodes for a second enzyme.